

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB# \_\_\_\_\_

Mailbox  
12E12

Requester's Full Name: Anne-Marie Baker Examiner #: 74977 Date: 4/18/01  
Art Unit: 1632 Phone Number 306-9155 Serial Number: 08/963,288  
Mail Box and Bldg/Room Location: 12D07 Results Format Preferred (circle):  PAPER  DISK  E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Expression Vector

Inventors (please provide full names): Norstedt et al

Earliest Priority Filing Date: 10/19/95

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

- Please perform an ~~all~~ search for

TTCTGAGAA

Limit to 12mer or smaller.

POINT OF CONTACT:

BARB O'BRYEN

TECH. INFORMATION SPECIALIST  
STIC CM1 12C14 308-4291

- Claim is directed to an enhancer element consisting essentially of the nucleotide sequence.

- There is no CRF for this and thus no SEQ ID No. for this 9-nucleotide sequence because the sequence rules apply to sequences 10-nucleotides or longer. Thus, this case is not required to comply with the sequence rules. Or, looked at another way, the case is in compliance because no CRF is required.

STAFF USE ONLY

Type of Search Vendors and cost where applicable

Searcher: <u>BAB</u>	NA Sequence (#): <u>1</u>	STN _____
Searcher Phone #:	AA Sequence (#):	Dialog _____
Searcher Location:	Structure (#):	Questel/Orbit _____
Date Searcher Picked Up: <u>4-18-01</u>	Bibliographic	Dr. Link _____
Date Completed: <u>4-23-01</u>	Litigation	Lexis/Nexis _____
Searcher Prep & Review Time: <u>20</u>	Fulltext	Sequence Systems <u>IG, Et alias 03</u>
Clerical Prep Time:	Patent Family	WWW/Internet _____
Online Time: <u>15</u>	Other	Other (specify)

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QY 1 ttctggaaa 9  
 US-08-369-796-34/C  
 Sequence 34, Application US/08369796  
 Patent No. 5716622  
 Db 9 TTCTGAGAA 1

RESULT 2  
 US-08-369-796-34/C  
 Sequence 34, Application US/08369796  
 Patent No. 5716622  
 GENERAL INFORMATION:  
 APPLICANT: James E. Darnell, Jr.  
 APPLICANT: Zilong Wen  
 APPLICANT: Curt M. Horvath  
 APPLICANT: Zhong Zhong  
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 08/228,935  
 FILING DATE: 27-MAR-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/410,779B  
 FILING DATE: 14-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JURGENSEN, THOMAS E  
 REGISTRATION NUMBER: 34 195  
 REFERENCE/DOCKET NUMBER: 016-0013A.US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 550-7675  
 TELEFAX: (619) 533-3906  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: />desc = "OTHER NUCLEIC ACID,"  
 DESCRIPTION: SYNTHETIC DNA,  
 US-08-410-779B-35

Query Match 100.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+07; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctggaaa 9  
 Db 9 TTCTGAGAA 1

RESULT 4  
 US-08-852-091-34/C  
 Sequence 34, Application US/08852091  
 Patent No. 5803228  
 GENERAL INFORMATION:  
 APPLICANT: James E. Darnell, Jr.  
 APPLICANT: Zilong Wen  
 APPLICANT: Curt M. Horvath  
 APPLICANT: Zhong Zhong  
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/852,091  
 FILING DATE: 06-MAY-1997

Query Match 100.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+07; Mismatches 0; Indels 0; Gaps 0;  
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QY 1 ttctggaaa 9  
 Db 9 TTCTGAGAA 1

RESULT 3  
 US-08-410-779B-35/C  
 Sequence 35, Application US/08410779B  
 Patent No. 5804517  
 GENERAL INFORMATION:  
 APPLICANT: SEIDEL, H. MARTI  
 APPLICANT: LAMB, I. PETER  
 TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS  
 NUMBER OF SEQUENCES: 166  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED  
 STREET: 9393 TOWNE CENTRE DRIVE  
 CITY: SAN DIEGO  
 STATE: CALIFORNIA  
 COUNTRY: US  
 ZIP: 92121

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 08/228,935  
 FILING DATE: 27-MAR-1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/410,779B  
 FILING DATE: 14-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JURGENSEN, THOMAS E  
 REGISTRATION NUMBER: 34 195  
 REFERENCE/DOCKET NUMBER: 016-0013A.US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 550-7675  
 TELEFAX: (619) 533-3906  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: />desc = "OTHER NUCLEIC ACID,"  
 DESCRIPTION: SYNTHETIC DNA,  
 US-08-410-779B-35

Query Match 100.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+07; Mismatches 0; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctggaaa 9  
 Db 9 TTCTGAGAA 1

RESULT 4  
 US-08-852-091-34/C  
 Sequence 34, Application US/08852091  
 Patent No. 5803228  
 GENERAL INFORMATION:  
 APPLICANT: James E. Darnell, Jr.  
 APPLICANT: Zilong Wen  
 APPLICANT: Curt M. Horvath  
 APPLICANT: Zhong Zhong  
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/852,091  
 FILING DATE: 06-MAY-1997

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GenCore version 4.5  
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On nucleic - nucleic search, using sw model

Run on: April 21, 2001, 12:13:27 ; Search time 80.36 Seconds  
(without alignments)  
19.555 Million cell updates/sec

Title: SHORT  
perfect score: 9  
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 8730134 residues

Total number of hits satisfying chosen parameters: 23618

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cggn2\_6/ptodata/2/ina/5A\_COMB.seq: \*
- 2: /cggn2\_6/ptodata/2/ina/5B\_COMB.seq: \*
- 3: /cggn2\_6/ptodata/2/ina/6A\_COMB.seq: \*
- 4: /cggn2\_6/ptodata/2/ina/6B\_COMB.seq: \*
- 5: /cggn2\_6/ptodata/2/ina/PCTUS.COMB.seq: \*
- 6: /cggn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
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C 2	9	100.0	9 1	US-08-411-020-13
C 3	9	100.0	9 1	US-08-410-798-35
C 4	9	100.0	9 2	US-08-852-091-34
C 5	9	100.0	9 5	PCT-US95-0477-35
C 6	9	100.0	9 5	PCT-US95-17025-34
C 7	8	88.9	10 1	US-08-440-7878-85
C 8	8	88.9	10 1	US-08-440-7878-86
C 9	7.4	82.2	9 1	US-08-268-799-3
C 10	7.4	82.2	9 1	US-08-411-020-12
C 11	7.4	82.2	9 1	US-08-411-020-12
C 12	7.4	82.2	9 1	US-08-411-020-13
C 13	7.4	82.2	9 1	US-08-369-796-31
C 14	7.4	82.2	9 1	US-08-369-796-34
C 15	7.4	82.2	9 1	US-08-369-796-36
C 16	7.4	82.2	9 1	US-08-369-796-38
C 17	7.4	82.2	9 1	US-08-410-798-31
C 18	7.4	82.2	9 1	US-08-410-798-35
C 19	7.4	82.2	9 1	US-08-410-7798-51
C 20	7.4	82.2	9 1	US-08-410-7798-51
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C 22	7.4	82.2	9 2	US-08-852-091-34
C 23	7.4	82.2	9 2	US-08-852-091-36
C 24	7.4	82.2	9 2	US-08-852-091-38
C 25	7.4	82.2	9 3	US-08-873-709-6
C 26	7.4	82.2	9 5	PCT-US95-04477-31
C 27	7.4	82.2	9 5	PCT-US95-04477-35

**ALIGNMENTS**

RESULT 1  
US-08-411-020-13/C  
Sequence 13, Application US/08411020  
; Patent No. 571209  
; GENERAL INFORMATION:  
; APPLICANT: SEIDEL, H. MARTI  
; APPLICANT: LAMB, I. PETER  
; APPLICANT: CHAN, SHIN-SHY TIAN  
; TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR  
; DETECTING MODULATORS OF CYTOKINE ACTION  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ligand Pharmaceuticals Incorporated  
; STREET: 9933 Towne Centre Drive  
; CITY: San Diego  
; STATE: California  
; COUNTRY: US  
ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/411,020  
FILING DATE: 27-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jurgensen, Thomas E.  
REGISTRATION NUMBER: 34,195  
REFERENCE/DOCKET NUMBER: 016-0030.US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-3966  
TELEFAX: (619) 535-3966  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
SEQUENCE LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLogy: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
DESCRIPTION: SYNTHETIC DNA,"  
US-08-411-020-13

Query Match 100.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. 1.9e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctggaaaa 9  
   |||||  
   9 TTCTGGAGAA 1

RESULT 2  
 US-08-369-796-34/c  
 Sequence 34, Application US/08369796  
 Patent No. 5716622  
 GENERAL INFORMATION:  
 APPLICANT: James E. Darnell, Jr.  
 APPLICANT: Zilong Wen  
 APPLICANT: Curt M. Horvath  
 APPLICANT: Zhong Zhong  
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 08/228, 935  
 FILING DATE: 14-APR-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-116  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,"  
 US-08-410-779B-35

RESULT 4  
 US-08-852-091-34/c  
 Sequence 34, Application US/08852091  
 Patent No. 5883228  
 GENERAL INFORMATION:  
 APPLICANT: James E. Darnell, Jr.  
 APPLICANT: Zilong Wen  
 APPLICANT: Curt M. Horvath  
 APPLICANT: Zhong Zhong  
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/852, 091  
 FILING DATE: 06-MAY-1997

ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED  
 STREET: 9393 TOWNE CENTRE DRIVE  
 CITY: SAN DIEGO  
 STATE: CALIFORNIA  
 COUNTRY: US  
 ZIP: 92121

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/410, 779B  
 FILING DATE: 27-MAR-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: JURGENSEN, THOMAS E  
 REGISTRATION NUMBER: 34,195  
 REFERENCE/DOCKET NUMBER: 016-0013A.US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 550-7675  
 TELEX: (619) 535-3906  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,"  
 US-08-410-779B-35

Query Match 100.0%; Score 9; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query 1 ttctggaaaa 9  
 Db 9 TTCTGGAGAA 1

RESULT 3  
 US-08-410-779B-35/c  
 Sequence 35, Application US/08410779B  
 Patent No. 5814517  
 GENERAL INFORMATION:  
 APPLICANT: SEIDEL, H. MARTI  
 APPLICANT: LAMB, I. PETER  
 TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS  
 TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE  
 NUMBER OF SEQUENCES: 166  
 CORRESPONDENCE ADDRESS:

CLASSIFICATION: 424  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/369,796  
 FILING DATE: 06-JAN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-116  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA synthetic probe  
 HYPOTHETICAL: NO  
 US-08-852-091-34

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Query Match 100.0%; Score 9; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ttctggaa 9  
 Db 9 TTCTGAGAA 1

RESULT 5  
 PCT-US95-04477-35/c

GENERAL INFORMATION:  
 APPLICANT: Sequence 35, Application PC/US9504477

APPLICANT: ;  
 TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE

NUMBER OF SEQUENCES: 165

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/17025  
 FILING DATE: 28-DEC-1995  
 CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/369,796  
 FILING DATE: 06-JAN-1995  
 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-116  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA synthetic probe  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 PCT-US95-17025-34

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Query Match 100.0%; Score 9; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ttctggaa 9  
 Db 9 TTCTGAGAA 1

RESULT 7  
 US-08-440-787A-85/c  
 Sequence 85, Application US/08440787A  
 Patent No. 577034

GENERAL INFORMATION:  
 APPLICANT: Huie, William D.  
 TITLE OF INVENTION: Soluble Peptides Having Constrained, Secondary Conformation in Solution and Method of Making  
 TITLE OF INVENTION: Same.  
 NUMBER OF SEQUENCES: 174

RESPONSE ADDRESS:  
 ADDRESSEE: Campbell & Flores LLP



**Matches** 8; **Conservative** 0; **Mismatches** 1; **Indels** 0; **Gaps** 0;

**RESULT** 10  
**S-08-411-020-12**  
**Sequence** 12, Application US/08411020  
**Patent No.** 5712094  
**GENERAL INFORMATION:**  
**APPLICANT:** SEIDEL, H. MARTI  
**APPLICANT:** LAMB, T. PETER  
**APPLICANT:** CHAN, SHIN-SHAY TIAN  
**TITLE OF INVENTION:** METHODS AND ASSOCIATED REAGENTS FOR DETECTING MODULATORS OF CYTOKINE ACTION  
**TITLE OF INVENTION:** DETECTING MODULATORS OF CYTOKINE ACTION  
**NUMBER OF SEQUENCES:** 59

**CORRESPONDENCE ADDRESS:**  
**ADDRESSEE:** Ligand Pharmaceuticals Incorporated  
**STREET:** 9393 Towne Centre Drive  
**CITY:** San Diego  
**STATE:** California  
**COUNTRY:** US  
**ZIP:** 92121

**COMPUTER READABLE FORM:**  
**MEDIUM TYPE:** Floppy disk  
**COMPUTER:** IBM PC compatible  
**OPERATING SYSTEM:** PC-DOS/MS-DOS  
**SOFTWARE:** PatentIn Release #1.0, Version #1.30

**APPLICATION NUMBER:** US/08/411,020  
**FILING DATE:** 27-MAR-1995  
**CLASSIFICATION:** 435

**ATTORNEY/AGENT INFORMATION:**  
**NAME:** Jurgensen, Thomas E.  
**REGISTRATION NUMBER:** 34,195

**REFERENCE/DOCKET NUMBER:** 016-0030.US  
**TELECOMMUNICATION INFORMATION:**  
**TELEPHONE:** (619) 550-7675  
**TELEFAX:** (619) 535-3906

**INFORMATION FOR SEQ ID NO:** 12:  
**SEQUENCE CHARACTERISTICS:**  
**LENGTH:** 9 base pairs  
**TYPE:** nucleic acid  
**STRANDEDNESS:** single  
**TOPOLOGY:** linear  
**MOLECULE TYPE:** other nucleic acid  
**DESCRIPTION:** /desc = "OTHER NUCLEIC ACID",  
**DESCRIPTION:** SYNTHETIC DNA

**US-08-411-020-12**

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**Query Match** 82.2%; **Score** 7.4; **DB** 1; **Length** 9;  
**Best Local Similarity** 88.9%; **Pred.** No. 1.9e+07; **Mismatches** 1; **Indels** 0; **Gaps** 0;

**RESULT** 12  
**US-08-411-020-13**  
**Sequence** 13, Application US/08411020  
**Patent No.** 5712094  
**GENERAL INFORMATION:**  
**APPLICANT:** SEIDEL, H. MARTI  
**APPLICANT:** LAMB, T. PETER  
**APPLICANT:** CHAN, SHIN-SHAY TIAN  
**TITLE OF INVENTION:** METHODS AND ASSOCIATED REAGENTS FOR DETECTING MODULATORS OF CYTOKINE ACTION  
**NUMBER OF SEQUENCES:** 59

**CORRESPONDENCE ADDRESS:**  
**ADDRESSEE:** Ligand Pharmaceuticals Incorporated  
**STREET:** 9393 Towne Centre Drive  
**CITY:** San Diego  
**STATE:** California  
**COUNTRY:** US  
**ZIP:** 92121

**COMPUTER READABLE FORM:**  
**MEDIUM TYPE:** Floppy disk  
**COMPUTER:** IBM PC compatible  
**OPERATING SYSTEM:** PC-DOS/MS-DOS  
**SOFTWARE:** PatentIn Release #1.0, Version #1.30

**CURRENT APPLICATION DATA:**  
**APPLICATION NUMBER:** US/08/411,020  
**FILING DATE:** 27-MAR-1995  
**CLASSIFICATION:** 435

**ATTORNEY/AGENT INFORMATION:**  
**NAME:** Jurgensen, Thomas E.  
**REGISTRATION NUMBER:** 34,195

**REFERENCE/DOCKET NUMBER:** 016-0030.US  
**TELECOMMUNICATION INFORMATION:**  
**TELEPHONE:** (619) 550-7675  
**TELEFAX:** (619) 535-3906

**INFORMATION FOR SEQ ID NO:** 12:  
**SEQUENCE CHARACTERISTICS:**  
**LENGTH:** 9 base pairs  
**TYPE:** nucleic acid  
**STRANDEDNESS:** single  
**TOPOLOGY:** linear  
**MOLECULE TYPE:** other nucleic acid  
**DESCRIPTION:** /desc = "OTHER NUCLEIC ACID",  
**DESCRIPTION:** SYNTHETIC DNA

**US-08-411-020-12**

---

**Query Match** 82.2%; **Score** 7.4; **DB** 1; **Length** 9;  
**Best Local Similarity** 88.9%; **Pred.** No. 1.9e+07; **Mismatches** 1; **Indels** 0; **Gaps** 0;

**Matches** 8; **Conservative** 0; **Mismatches** 1; **Indels** 0; **Gaps** 0;

**S-08-411-020-12**

---

**Query Match** 82.2%; **Score** 7.4; **DB** 1; **Length** 9;  
**Best Local Similarity** 88.9%; **Pred.** No. 1.9e+07; **Mismatches** 1; **Indels** 0; **Gaps** 0;

**Matches** 8; **Conservative** 0; **Mismatches** 1; **Indels** 0; **Gaps** 0;

**S-08-411-020-12**

---

**RESULT** 11  
**S-08-411-020-12/c**  
**Sequence** 12, Application US/08411020  
**Patent No.** 5712094  
**GENERAL INFORMATION:**  
**APPLICANT:** SEIDEL, H. MARTI  
**APPLICANT:** LAMB, T. PETER  
**APPLICANT:** CHAN, SHIN-SHAY TIAN  
**TITLE OF INVENTION:** METHODS AND ASSOCIATED REAGENTS FOR DETECTING MODULATORS OF CYTOKINE ACTION  
**NUMBER OF SEQUENCES:** 59

**CORRESPONDENCE ADDRESS:**  
**ADDRESSEE:** Ligand Pharmaceuticals Incorporated  
**STREET:** 9393 Towne Centre Drive  
**CITY:** San Diego  
**STATE:** California  
**COUNTRY:** US  
**ZIP:** 92121

**COMPUTER READABLE FORM:**  
**MEDIUM TYPE:** Floppy disk  
**COMPUTER:** IBM PC compatible  
**OPERATING SYSTEM:** PC-DOS/MS-DOS  
**SOFTWARE:** PatentIn Release #1.0, Version #1.30

**CURRENT APPLICATION DATA:**  
**APPLICATION NUMBER:** US/08/411,020  
**FILING DATE:** 27-MAR-1995  
**CLASSIFICATION:** 435

**ATTORNEY/AGENT INFORMATION:**  
**NAME:** Jurgensen, Thomas E.

REGISTRATION NUMBER: 34,195  
 REFERENCE/DOCKET NUMBER: 016-0030.US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-3906  
 TELEFAX: (619) 550-7675  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
 DESCRIPTION: SYNTHETIC DNA,"  
 US-08-411-020-13

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+07; 1; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 1; Db 0; Gaps 0;

Qy 1 ttctggaa 9  
 Db 9 TTCTGGAA 1

RESULT 13  
 US-08-369-796-31/C  
 ; Sequence 31, Application US/08369796  
 ; Patent No. 5716622

GENERAL INFORMATION:  
 APPLICANT: James E. Darnell, Jr.  
 APPLICANT: Zilong Wen  
 APPLICANT: Curt M. Horvath  
 APPLICANT: Zhong Zhong

TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL NUMBER OF SEQUENCES: 39

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patient Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/369,796  
 FILING DATE: 06-JAN-1995  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-116

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEX: 133521  
 TELEFAX: 201 343-1684

INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA synthetic probe  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-369-796-34

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+07; 1; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 1; Db 0; Gaps 0;

Qy 1 ttctggaa 9  
 Db 9 TTCTGGAA 1

RESULT 14  
 US-08-369-796-34  
 ; Sequence 34, Application US/08369796  
 ; Patent No. 5716622

GENERAL INFORMATION:  
 APPLICANT: James E. Darnell, Jr.  
 APPLICANT: Zilong Wen  
 APPLICANT: Curt M. Horvath  
 APPLICANT: Zhong Zhong

TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patient Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/369,796  
 FILING DATE: 06-JAN-1995  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-116

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEX: 133521  
 TELEFAX: 201 343-1684

INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA synthetic probe  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-369-796-34

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+07; 1; Indels 0; Gaps 0;  
 Matches 8; Conservative 0; Mismatches 1; Db 0; Gaps 0;

Qy 1 ttctggaa 9  
 Db 9 TTCTGGAA 1

RESULT 15  
 US-08-369-796-36/C  
 ; Sequence 36, Application US/08369796  
 ; Patent No. 5716622

GENERAL INFORMATION:  
 APPLICANT: James E. Darnell, Jr.

APPLICANT: Zilong Wen  
APPLICANT: Curt M. Horvath  
APPLICANT: Zhong Zhong  
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
NUMBER OF SEQUENCES: 39

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US08/369,796  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-116

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

## INFORMATION FOR SEQ ID NO: 36:

## SEQUENCE CHARACTERISTICS:

LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA synthetic probe  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-369-796-36

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1 9e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 ttctttagaa 9
Db	9 TTCCGAGAA 1

Search completed: April 21, 2001, 13:12:32  
Job time: 3545 sec

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GenCore version 4.5  
copyright (c) 1993 - 2000 Compugen Ltd.

Om nucleic - nucleic search, using sw model

Run on: April 21, 2001, 12:14:34 ; Search time 110.76 Seconds  
(without alignments)  
47.436 Million cell updates/sec

Title: SHORT  
perfect score: 9  
Sequence: ttctgagaa 9

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 65774

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_0401:\*

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4: /SIDS2/gcgdata/geneseq/geneseq/NAI1984.DAT: \*  
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10: /SIDS2/gcgdata/geneseq/geneseq/NAI1990.DAT: \*  
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12: /SIDS2/gcgdata/geneseq/geneseq/NAI1992.DAT: \*  
13: /SIDS2/gcgdata/geneseq/geneseq/NAI1993.DAT: \*  
14: /SIDS2/gcgdata/geneseq/geneseq/NAI1994.DAT: \*  
15: /SIDS2/gcgdata/geneseq/geneseq/NAI1995.DAT: \*  
16: /SIDS2/gcgdata/geneseq/geneseq/NAI1996.DAT: \*  
17: /SIDS2/gcgdata/geneseq/geneseq/NAI1997.DAT: \*  
18: /SIDS2/gcgdata/geneseq/geneseq/NAI1998.DAT: \*  
19: /SIDS2/gcgdata/geneseq/geneseq/NAI1999.DAT: \*  
20: /SIDS2/gcgdata/geneseq/geneseq/NAI2000.DAT: \*  
21: /SIDS2/gcgdata/geneseq/geneseq/NAI2001.DAT: \*22: /SIDS2/gcgdata/geneseq/geneseq/NAI2001.DAT: \*pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Length	DB ID	Description
C 1	9	100.0	9 16 T4149	Cytokine responsive
C 2	9	100.0	9 17 T41583	Cytokine activated
C 3	9	100.0	9 17 V5876	Regulatory element
C 4	8	88.9	11 20 X77642	Regulatory element Nil active EGS 6.
C 5	7.4	82.2	9 14 Q5424	SIVmac-HIV-1 Junc
C 6	7.4	82.2	9 15 T4165	Cytokine responsive
C 7	7.4	82.2	9 16 T4165	Cytokine responsive
C 8	7.4	82.2	9 16 T4149	Cytokine responsive
C 9	7.4	82.2	9 16 T4145	Cytokine activated
C 10	7.4	82.2	9 17 T41582	Cytokine activated
C 11	7.4	82.2	9 17 T41582	Cytokine activated

**ALIGNMENTS**

RESULT ID	NAME	TYPE	SEQUENCE	DESCRIPTION
T4149/C	T4149 standard; DNA; 9 BP.	XX		
T4149;		AC		
		XX		
	29-MAY-1996 (first entry)	DT		
		XX		
	Cytokine responsive DNA spacer regulatory element.	DE		
	Regulatory element; transcriptional regulatory protein; signalling molecule; DNA spacer; agonist; antagonist; anaemia; gene transcription; inflammation; cytopenia; ss.	KW		
	Synthetic.	OS		
	W09528482-A2.	PN		
	26-OCT-1995.	PD		
	26-OCT-1995.	PF		
	10-APR-1995; 95NO-US04477.	PF		
	XX	PR	27-MAR-1995; 95US-0410780.	Cytokine activated
	XX	PR	14-APR-1994; 94US-0228935.	Regulatory element
	XX	PA	(LIGA-) LIGAND PHARM INC.	Regulatory element
	XX	PA	Lamb IP, Seidel HM;	Regulatory element
	XX	DR	WPI; 1995-373797/48.	Regulatory element
	XX	PT	DNA spacer regulatory elements responsive to cytokine(s) - for detecting the presence of transcriptional regulatory protein in a sample	Regulatory element

XX  
 PS Claim 7; Page 125; 135pp; English.  
 XX  
 CC The present oligonucleotide comprises a regulatory element  
 CC  $T^x(N_x)AA$ , where  $x$  is 4-7, and the regulatory element binds an  
 CC activated transcriptional regulatory protein in response to a  
 CC signalling mol., i.e. a cytokine. This cytokine responsive DNA  
 CC spacer regulatory element can be used to detect the presence of  
 CC a transcriptional regulatory protein in a sample, and in assays  
 CC for (anti)agonists of gene transcription. The identified cpds.  
 CC may be used to treat cytokine-induced disease states, or to  
 CC ameliorate disease states caused by cytokine deficiency, e.g.  
 CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.  
 XX SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 ID 1 ttctggaa 9  
 Db 9 TTCTGAGAA 1

RESULT 2  
 T41583/C  
 ID 141583 standard; DNA; 9 BP.  
 XX AC T41583;  
 DT 04-JUN-1997 (first entry)  
 XX DE Cytokine activated STAT protein dependent DNA regulatory element.  
 KW Regulatory element; protein; cytokine; responsive; host cell;  
 KW transfection; agonist; antagonist; mediated; transcription;  
 KW modulation; STAT; STAT5; STAT6; signalling pathway; ss.  
 XX OS Synthetic.  
 XX PN W09630515-A1.  
 XX PD 03-OCT-1996.  
 XX PF 25-MAR-1996; 96WO-US04012.  
 XX PR 27-MAR-1995; 95US-0410779.  
 XX DR 29-SEP-1998.  
 XX PT 27-MAR-1995; 95US-0410779.  
 XX PR 14-APR-1994; 94US-0228935.  
 XX PA (LIGA-) LIGAND PHARM INC.  
 XX PI Lamb IP, Seidel HM;  
 XX DR WPI; 1998-541763/46;  
 XX PT DNA constructs containing cytokine-responsive regulatory elements -  
 PT useful in assays for transcription-regulating proteins or gene  
 PT transcription agonists or antagonists  
 XX Disclosure; Column 11; 58pp; English.

XX PS V56842-v56976 and V61601-v61631 are oligonucleotides used in the  
 CC production of constructs comprising a cytokine-responsive regulatory  
 CC element linked to a promoter which is linked to a heterologous coding  
 CC sequence so that the coding sequence is under the transcriptional control  
 CC of the regulatory element and the promoter, where the regulatory element  
 CC has a nucleotide sequence selected from T $C$ NNNN, T $N$ NYTA, and T $C$ NYTA  
 CC where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to  
 CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,  
 CC in a sample by contacting the sample with the construct so that the  
 CC protein binds to the regulatory element, and detecting or separating the  
 CC resulting complex. The cells can be used in screening assays for agonists  
 CC of gene transcription, in which the level of expression of the coding  
 CC sequence is measured in the presence and absence of a test compound or  
 CC in the presence of the corresponding cytokine.  
 XX SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC cytokine modulators involved in the STAT5 and/or STAT protein  
 CC signalling pathway.  
 XX Sequence 9 BP; 3 A; 2 C; 1 G; 3.T; 0 other;  
 XX SQ Query Match 100.0%; Score 9; DB 17; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctggaa 9  
 Db 9 TTCTGAGAA 1

RESULT 3  
 V56876/C  
 ID V56876 standard; DNA; 9 BP.  
 XX AC V56876;  
 DT 02-DEC-1998 (first entry)  
 DE Regulatory element containing oligonucleotide #35.  
 KW Cytokine-responsive regulatory; primer; promoter; detection; isolation;  
 KW transcriptional control; STAT protein; screening; agonist; ss.  
 XX OS Synthetic.  
 XX PN US5814517-A.  
 XX PD 29-SEP-1998.  
 XX PT 27-MAR-1995; 95US-0410779.  
 XX PR 14-APR-1994; 94US-0228935.  
 XX PA (LIGA-) LIGAND PHARM INC.  
 XX PI Lamb IP, Seidel HM;  
 XX DR WPI; 1998-541763/46;  
 XX PT DNA constructs containing cytokine-responsive regulatory elements -  
 PT useful in assays for transcription-regulating proteins or gene  
 PT transcription agonists or antagonists  
 XX Disclosure; Column 11; 58pp; English.

XX PS V56842-v56976 and V61601-v61631 are oligonucleotides used in the  
 CC production of constructs comprising a cytokine-responsive regulatory  
 CC element linked to a promoter which is linked to a heterologous coding  
 CC sequence so that the coding sequence is under the transcriptional control  
 CC of the regulatory element and the promoter, where the regulatory element  
 CC has a nucleotide sequence selected from T $C$ NNNN, T $N$ NYTA, and T $C$ NYTA  
 CC where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to  
 CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,  
 CC in a sample by contacting the sample with the construct so that the  
 CC protein binds to the regulatory element, and detecting or separating the  
 CC resulting complex. The cells can be used in screening assays for agonists  
 CC of gene transcription, in which the level of expression of the coding  
 CC sequence is measured in the presence and absence of a test compound or  
 CC in the presence of the corresponding cytokine.  
 XX SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 19; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+07;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC a novel DNA construct comprises an oligonucleotide (ON) comprising  
 CC a regulatory element having the present sequence, operably linked  
 CC to a promoter, which is operably linked to a heterologous gene  
 CC (preferably a marker gene). The gene is under the transcriptional  
 CC control of the promoter and the ON sequence when the ON is bound by  
 CC a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,  
 CC erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,  
 CC IL-13 or IL-15. Cytokine responsive host cells transfected with the  
 CC DNA construct can be used to measure the ability of a compound to  
 act as an agonist or antagonist of cytokine mediated gene  
 transcription. In particular, they can be used to screen for

QY 1 ttctggagaa 9  
   |||||||  
   9 TCTGAGAA 1

RESULT 4  
 XX X77642/C  
 ID X77642 standard; DNA; 11 BP.  
 XX  
 AC X77642;  
 XX  
 DT 09-AUG-1999 (first entry)  
 XX  
 DE NIL active EGS 6.  
 XX  
 KW External guide sequence; EGS; target mRNA; identification; diagnostic;  
 XX inactivation; essential gene; therapy; ss.  
 XX  
 OS Synthetic.  
 XX WO9927135-A2.  
 XX  
 PD 03-JUN-1999.  
 XX  
 PF 20-NOV-1998; 98WO-US24854.  
 XX  
 PR 30-MAR-1998; 98US-0079851.  
 PR 21-NOV-1997; 97US-0976220.  
 PA (INNO-) INNOVIR LAB INC.  
 XX  
 PT Kindt TJ, Nilsen TW, Robertson HD;  
 XX  
 DR WPI; 1999-357853/30.

PT Identifying and inhibiting functional nucleic acid molecules in  
 PT cells  
 PS Example 3; Page 28; 58pp; English.

XX  
 CC this invention describes a novel method allowing essential or functional  
 CC genes to be rapidly identified and inactivated. The method is able to  
 firstly identify most of the essential genes in an organism (i.e. a  
 CC bacteria or a eukaryote) needed for survival, and secondly it provides  
 CC for reducing or inactivating their expression. The method is able to  
 identify functional oligonucleotide molecules able to be used as  
 CC diagnostic reagents and therapeutics. The method provides a means for  
 identifying essential genes whose sequence is known only as part of a  
 CC genome with unknown function, as well as a means for identifying  
 functional oligonucleotide molecules. The method involves the use of a  
 CC nucleic acid molecule comprising (a) a first reporter gene encoding a  
 CC fusion protein comprising a protein of interest (itself translated from  
 CC an RNA of interest) and a reporter protein, (b) a second reporter gene  
 CC encoding a second reporter protein, and (c) a targeting gene encoding a  
 CC functional oligonucleotide molecule such as an external guide sequence  
 CC (EGS), a ribozyme or an antisense RNA and targeted to the RNA of interest  
 CC at a site on the first reporter gene able to encode the RNA of interest.  
 XX  
 Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 other;

SQ Query Match 88.9%; Score 8; DB 20; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctggagaa 8  
   |||||||  
   9 TCTGAGAA 2

RESULT 5  
 ID Q53424/c  
 Q53424 standard; DNA; 9 BP.

XX XX 053424;  
 AC XX  
 XX DT 16-JUN-1994 (first entry)  
 XX DE SIVmac/HIV-1 junction region #3.  
 XX Junction fragment; vector; simian immunodeficiency virus; SIV; gag;  
 KW pol; vif; vpx; long terminal repeat; LTR; HIV-1; env; tat; rev;  
 KW nef; vpr; chimeric virus; replication competent; monkey; mandrill;  
 KW macaque; disease progression; vaccine; epitope; immune response;  
 KW envelope glycoprotein; cytotoxic T lymphocyte; ss.  
 XX OS Synthetic.  
 XX PN WO9324632-A.  
 XX PD 09-DEC-1993.  
 XX PF 20-MAY-1993; 93WO-US04814.  
 XX PR 22-MAY-1992; 92US-0887505.  
 XX PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (HARD ) HARVARD COLLEGE.  
 XX PI Haseltine WA, Letvin N, Li J, Sodroski J;  
 XX DR WPI; 1993-405823/50.

XX PT Hybrid SIV-HIV-1 viral vectors - used to provide animal models  
 PT for HIV-1 infection or a therapeutic agents or in vaccines for  
 PT HIV-1.

XX PS Disclosure; Fig 1C; 72pp; English.

CC The sequences given in 053422-28 represent junction fragments which  
 CC were used in the construction the vectors of the invention. These  
 CC vectors contain a 5' DNA segment which contains a sufficient number  
 CC of nucleotides corresponding to a simian immunodeficiency virus (SIV)  
 CC genome to encode a functional gag, pol, vif and vpx protein and has  
 CC a SIV long terminal repeat (LTR), and a 3' DNA segment which contains  
 CC a sufficient number of nucleotides corresponding to at least one  
 CC HIV-1 genome to encode a functional HIV-1 env, tat and rev protein  
 CC and a sufficient number of nucleotides corresponding to a SIV genome  
 CC to encode a functional nef protein and has a SIV LTR. The vector  
 CC further comprises a sufficient number of nucleotides corresponding to  
 CC the SIV genome to encode a functional SIV vpr protein. Vectors such  
 CC as these produce chimeric viruses containing HIV-1 components. As a  
 CC result of transfecting cells with these vectors, replication competent  
 CC viruses that are infectious in animal systems such as monkeys, eg.  
 CC mandrills, macaques, etc. can be produced. The vectors can be used for  
 CC creating an animal model for studying disease progression by HIV-1,  
 CC for screening for compounds exhibiting anti-HIV activity, for screening  
 CC for a vaccine against HIV infection and for determining the specific  
 CC epitopes of a HIV-1 envelope glycoprotein recognised by cytotoxic T  
 CC lymphocytes. They can also be used to boost immune response in a HIV  
 CC infected individual or as a vaccine to prevent infection.

SQ Sequence 9 BP; 3 A; 1 C; 1 G; 4 T; 0 other;

Query Match 82.2%; Score 7.4; DB 14; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 6.5e+07;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctggagaa 9  
   |||||||  
   9 TCTGAGAA 1

RESULT 6  
 ID T14165



XX  
DR  
XX  
PT DNA spacer regulatory elements responsive to cytokine(s) - for  
PT detecting the presence of transcriptional regulatory protein in a  
sample  
XX  
PS Claim 7; Page 125; 135pp; English.

CC The present oligonucleotide comprises a regulatory element  
CC  $\text{Tr}(\text{NxRA})$ , where  $\text{x}$  is 4-7, and the regulatory element binds an  
activated transcriptional regulatory protein in response to a  
signalling mol., i.e. a cytokine. This cytokine responsive DNA  
spacer regulatory element can be used to detect the presence of  
a transcriptional regulatory protein in a sample, and in assays  
for (ant)agonists of gene transcription. The identified cpds.  
may be used to treat cytokine-induced disease states, or to  
ameliorate disease states caused by cytokine deficiency, e.g.  
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.  
XX Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 82.2%; Score 7.4; DB 16; Length 9;  
Best Local Similarity 88.9%; Pred. No. 6.5e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ttctggaa 9  
Db 1 ttctcgaa 9

RESULT 9  
T14145/C  
ID T14145 standard; DNA; 9 BP.  
XX  
AC T14145;  
DT 29-MAY-1996 (first entry)  
XX  
DE Cytokine responsive DNA spacer regulatory element.  
XX  
KW Regulatory element; transcriptional regulatory protein;  
signalling molecule; DNA spacer; agonist; antagonist; anaemia;  
gene transcription; inflammation; cytopenia; cancer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9528482-A2.  
XX  
PD 26-OCT-1995.  
XX  
PF 10-APR-1995; 95WO-US04477.  
XX  
PR 27-MAR-1995; 95US-0410780.  
PR 14-APR-1994; 94US-0228935.  
PA (LIGA-) LIGAND PHARM INC.  
XX  
PI Lamb IP; Seidel HM; Tian Chan S;  
XX  
DR WPI; 1995-455362/45.  
XX  
PT DNA construct for screening modulators of cytokine-mediated  
transcription - contg. regulatory element and a cytokine-sensitive  
PT promoter operably linked to a heterologous gene  
XX  
PS Claim 5; Page 61; 72pp; English.

XX  
CC A novel DNA construct comprises an oligonucleotide (ON) comprising  
CC a regulatory element having the present sequence, operably linked  
CC to a promoter, which is operably linked to a heterologous gene  
(preferably a marker gene). The gene is under the transcriptional  
control of the promoter and the ON sequence when the ON is bound by  
CC a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,  
CC erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,  
CC IL-13 or IL-15. Cytokine responsive host cells transfected with the  
DNA construct can be used to measure the ability of a compound to  
act as an agonist or antagonist of cytokine mediated gene  
CC transcription. In particular, they can be used to screen for  
CC cytokine modulators involved in the STAT5 and/or STAT6 protein  
CC signalling pathway.  
XX  
Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

XX  
Query Match 82.2%; Score 7.4; DB 17; Length 9;  
SQ

CC spacer regulatory element can be used to detect the presence of  
CC a transcriptional regulatory protein in a sample, and in assays  
for (ant)agonists of gene transcription. The identified cpds.  
CC may be used to treat cytokine-induced disease states, or to  
CC ameliorate disease states caused by cytokine deficiency, e.g.  
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.  
XX Sequence 9 BP; 3 A; 3 C; 1 G; 2 T; 0 other;

Query Match 82.2%; Score 7.4; DB 16; Length 9;  
Best Local Similarity 88.9%; Pred. No. 6.5e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ttctggaa 9  
Db 9 TTCGGGAA 1

RESULT 10  
T41582  
ID T41582 standard; DNA; 9 BP.  
XX  
AC T41582;  
DT 04-JUN-1997 (first entry)  
XX  
DE Cytokine activated STAT protein dependent DNA regulatory element.  
XX  
KW Regulatory element; Protein; cytokine; responsive; host cell;  
transfection; agonist; antagonist; mediated; transcription;  
modulation; STAT; STAT5; STAT6; signalling pathway; ss.  
XX  
OS Synthetic.  
XX  
PN WO9530515-A1.  
XX  
PD 03-OCT-1996.  
XX  
PF 25-MAR-1996; 96WO-US04012.  
XX  
PR 27-MAR-1995; 95US-0411020.  
PA (LIGA-) LIGAND PHARM INC.  
XX  
PI Lamb IP; Seidel HM; Tian Chan S;  
XX  
DR WPI; 1996-455362/45.  
XX  
PT DNA construct for screening modulators of cytokine-mediated  
transcription - contg. regulatory element and a cytokine-sensitive  
PT promoter operably linked to a heterologous gene  
XX  
PS Claim 5; Page 61; 72pp; English.

XX  
CC A novel DNA construct comprises an oligonucleotide (ON) comprising  
CC a regulatory element having the present sequence, operably linked  
CC to a promoter, which is operably linked to a heterologous gene  
(preferably a marker gene). The gene is under the transcriptional  
control of the promoter and the ON sequence when the ON is bound by  
CC a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,  
CC erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,  
CC IL-13 or IL-15. Cytokine responsive host cells transfected with the  
DNA construct can be used to measure the ability of a compound to  
act as an agonist or antagonist of cytokine mediated gene  
CC transcription. In particular, they can be used to screen for  
CC cytokine modulators involved in the STAT5 and/or STAT6 protein  
CC signalling pathway.  
XX  
Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

XX  
Query Match 82.2%; Score 7.4; DB 17; Length 9;

Qy	1 ttctggaa 9													
Db	1 ttctggaa 9													
RESULT	11													
T41582/C														
ID	T41582	standard; DNA; 9 BP.												
XX														
AC														
XX														
DT	04-JUN-1997	(first entry)												
XX														
DE	Cytokine activated STAT protein dependent DNA regulatory element.													
XX														
KW	Regulatory element; protein; cytokine; responsive; host cell; transfection; agonist; antagonist; mediated; transcription; modulation; STAT; STAT5; STAT6; signalling pathway; ss.													
XX														
OS	Synthetic.													
XX														
XX														
PR	W09630515-A1.													
XX														
PD	03-OCT-1996.													
XX														
PT	27-MAR-1996;	96WO-US040412.												
XX														
PR	27-MAR-1995;	95US-0411020.												
XX														
PA	(LIGA-) LIGAND PHARM INC.													
XX														
PI	Lamb IP, Seidel HM, Tian Chan S;													
XX														
DR	W09630515-A1.													
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XX														
PR	W09630515-A1.													
XX														
PT	03-OCT-1996.													
XX														
PR	27-MAR-1995;	95US-0411020.												
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PA	(LIGA-) LIGAND PHARM INC.													
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PI	Lamb IP, Seidel HM, Tian Chan S;													
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DR	W09630515-A1.													
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PR	W09630515-A1.													
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PT	03-OCT-1996.													
XX														
PR	27-MAR-1995;	95US-0411020.												
XX														
PA	(LIGA-) LIGAND PHARM INC.													
XX														
PI	Lamb IP, Seidel HM, Tian Chan S;													
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DR	W09630515-A1.													
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PR	27-MAR-1995;	95US-0411020.												
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PA	(LIGA-) LIGAND PHARM INC.													
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PI	Lamb IP, Seidel HM, Tian Chan S;													
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DR	W09630515-A1.													
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PR	03-OCT-1996.													
XX														
PR	27-MAR-1995;	95US-0411020.												
XX														
PA	(LIGA-) LIGAND PHARM INC.													
XX														
PI	Lamb IP, Seidel HM, Tian Chan S;													
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DR	W09630515-A1.													
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PA	(LIGA-) LIGAND PHARM INC.													
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PI	Lamb IP, Seidel HM, Tian Chan S;													
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PA	(LIGA-) LIGAND PHARM INC.													
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PI	Lamb IP, Seidel HM, Tian Chan S;													
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PA	(LIGA-) LIGAND PHARM INC.													
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PI	Lamb IP, Seidel HM, Tian Chan S;													
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XX														
PA	(LIGA-) LIGAND PHARM INC.													
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PA	(LIGA-) LIGAND PHARM INC.													
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PI	Lamb IP, Seidel HM, Tian Chan S;													
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PA	(LIGA-) LIGAND PHARM INC.													
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XX														
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PR	03-OCT-1996.													
XX														
PR	27-MAR-1995;	95US-0411020.												
XX														

XX	PN	US5814517-A.
XX	XX	(LIGA-) LIGAND PHARM INC.
PD	XX	Lamb IP, Seidel HM;
XX	XX	DR
PF	XX	WPT; 1998-541763/46.
XX	PF	27-MAR-1995; 95US-0410779.
PR	XX	27-MAR-1995; 95US-0410779.
PT	PR	14-APR-1994; 94US-0228935.
XX	PA	(LIGA-) LIGAND PHARM INC.
XX	XX	Lamb IP, Seidel HM;
PI	XX	DR
XX	DR	WPI; 1998-541763/46.
XX	PT	DNA constructs containing cytokine-responsive regulatory elements - useful in assays for transcription-regulating proteins or gene transcription agonists or antagonists
PT	XX	Disclosure; Column 12; 58PP; English.
PS	XX	Disclosure; column 12; 58PP; English.
PS	CC	V56842-V56976 and V61601-V61631 are oligonucleotides used in the production of constructs comprising a cytokine-responsive regulatory element linked to a promoter which is linked to a heterologous coding sequence so that the coding sequence is under the transcriptional control of the regulatory element and the promoter, where the regulatory element has a nucleotide sequence selected from TTCNNGA, TTYNYRA, and TTYNYYAA sequence so that the coding sequence is under the transcriptional control of the regulatory element and the promoter, where the regulatory element has a nucleotide sequence selected from TTCNNGA, TTYNYRA, and TTYNYYAA where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to detect or isolate transcription-regulating proteins, e.g. STAT proteins, protein binds to the regulatory element, and detecting or separating the resulting complex. The cells can be used in screening assays for agonists of gene transcription, in which the level of expression of the coding sequence is measured, in the presence and absence of a test compound or in a sample by contacting the sample with the construct so that the protein binds to the regulatory element, and detecting or separating the resulting complex. The cells can be used in screening assays for agonists of gene transcription, in which the level of expression of the coding sequence is measured in the presence and absence of a test compound or in the presence of the corresponding cytokine.
SQ	XX	Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;
Query Match	XX	Best Local Similarity 82.2%; Score 7.4; DB 19; Length 9; Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	CC	ttctggaaa 9             9
Db	CC	ttcttaagaa 9
RESULT	XX	14
V56892/-C	XX	V56892 standard; DNA; 9 BP.
ID	XX	V56876 standard; DNA; 9 BP.
AC	XX	V56876;
AC	XX	02-DEC-1998 (first entry)
AC	XX	Regulatory element containing oligonucleotide #35.
AC	XX	Cytokine-responsive regulatory; primer; promoter; detection; isolation; transcriptional control; STAT protein; screening; agonist; ss.
OS	XX	Synthetic.
OS	XX	US5814517-A.
DT	XX	02-DEC-1998 (first entry)
DE	XX	Regulatory element containing oligonucleotide #51.
XX	XX	Cytokine-responsive regulatory; primer; promoter; detection; isolation; transcriptional control; STAT protein; screening; agonist; ss.
KW	XX	Synthetic.
OS	XX	US5814517-A.
OS	XX	Lamb IP, Seidel HM;
OS	XX	DR
PF	XX	WPI; 1998-541763/46.
PF	XX	PT
PT	XX	DNA constructs containing cytokine-responsive regulatory elements - useful in assays for transcription-regulating proteins or gene transcription agonists or antagonists
PT	XX	useful in assays for transcription-regulating proteins or gene transcription agonists or antagonists
PT	XX	transcription agonists or antagonists
PT	XX	transcription agonists or antagonists

PS  
XX Disclosure; Column 11; 58pp; English.

CC V56842-V56976 and V61601-V61631 are oligonucleotides used in the  
CC production of constructs comprising a cytokine-responsive regulatory  
CC element linked to a promoter which is linked to a heterologous coding  
CC sequence so that the coding sequence is under the transcriptional control  
CC of the regulatory element and the promoter, where the regulatory element  
CC has a nucleotide sequence selected from TTCNNNNAA, TTYNYTAA, and TTYNYYAA  
CC where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to  
CC detect or isolate transcription-regulating proteins, e.g., STAT proteins,  
CC in a sample by contacting the sample with the construct so that the  
CC protein binds to the regulatory element, and detecting or separating the  
CC resulting complex. The cells can be used in screening assays for agonists  
CC of gene transcription, in which the level of expression of the coding  
CC sequence is measured in the presence and absence of a test compound or  
CC in the presence of the corresponding cytokine.  
XX

Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 82.2%; Score 7.4; DB 19; Length 9;  
Best Local Similarity 88.9%; Pred. No. 6 5e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Caps 0;  
Qy 1 ttctggaa 9  
Db 1 ttctcagaa 9

Search completed: April 21, 2001, 13:14:35  
Job time: 3601 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

April 21, 2001, 11:42:58 ; Search time 1240.49 Seconds

(without alignments) 44.677 Million cell updates/sec

Title: SHORT

Perfect score: 9

Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 15938

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : GenBank:\*

1: gb\_bal:\*

2: gb\_ba2:\*

3: gb\_ba3:\*

4: gb\_in1:\*

5: gb\_in2:\*

6: gb\_in3:\*

7: gb\_om:\*

8: gb\_ov:\*

9: gb\_pati:\*

10: gb\_pat2:\*

11: gb\_ph:\*

12: gb\_p11:\*

13: gb\_p12:\*

14: gb\_p13:\*

15: gb\_p14:\*

16: em\_b1:\*

17: em\_ba:\*

18: em\_fun:\*

19: em\_htgo\_hum:\*

20: em\_htgo\_inv:\*

21: em\_htgo\_rid:\*

22: em\_htgo\_hum1:\*

23: em\_htgo\_hum2:\*

24: em\_htgo\_hum3:\*

25: em\_htgo\_hum4:\*

26: em\_htgo\_hums:\*

27: em\_htgo\_hum7:\*

28: em\_htgo\_hum8:\*

29: em\_htgo\_hum9:\*

30: em\_htgo\_inv1:\*

31: em\_htgo\_inv2:\*

32: em\_htgo\_other:\*

Pred. No.	No.	%	Query	Length	DB	ID	Description
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	c 2	7.4	B	82.2	10	AR043683	AR043683 Sequence
	c 3	7.4	C	82.2	10	AR043683	AR043683 Sequence
	c 4	7.4	D	82.2	11	AR097294	AR097294 Sequence
	c 5	7.4	E	82.2	11	AX063653	AX063653 Sequence
	c 6	7.4	F	82.2	11	AX063656	AX063656 Sequence
	c 7	7.4	G	82.2	11	I39722	I39722 Sequence
	c 8	7.4	H	82.2	11	155839	155839 Sequence
	c 9	7.4	I	82.2	12	S75371	S75371 beta-hexosa
	c 10	7.4	J	82.2	12	93	
	c 11	7.8	K	82.2	12	S75371	S75371 beta-hexosa
			L	8	9	AR101594	AR101594 Sequence

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
32:						
33:						
34:						
35:						
36:						
37:						
38:						
39:						
40:						
41:						
42:						
43:						

RESULT 1  
 AX041991/c  
 LOCUS AX041991 9 bp DNA  
 DEFINITION Sequence 21 from Patent WO005067.  
 ACCESSION AX041991  
 VERSION AX041991.1 GI:11340754  
 KEYWORDS human.  
 SOURCE  
 ORGANISM Homo sapiens  
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 REFERENCE 1 (bases 1 to 9)  
 AUTHORS Nelson, P.S., Hood, L. and Lin, B.  
 TITLE Prostate-specific polynucleotides, polypeptides and their methods  
 of use  
 JOURNAL Patent: WO 005067-A 21 NOV-2000;  
 FEATURES Location/Qualifiers  
 source  
 BASE COUNT 3 a /bound\_moiety="Interleukin response element binding site"  
 ORIGIN

RESULT 2  
 AX043683  
 LOCUS AR043683 10 bp DNA  
 DEFINITION Sequence 53 from patent US 5814517.  
 ACCESSION AR043683  
 VERSION AR043683.1 GI:5964691  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Seidel, H. Martin and Lamb, I. Peter.  
 TITLE DNA spacer regulatory elements responsive to cytokines and methods for their use  
 JOURNAL Patent: US 5814517-A 29-SEP-1998;  
 FEATURES Location/Qualifiers  
 source 1..10 /organism="unknown" 1 g 4 t  
 BASE COUNT 4 a 1 c 1 g 4 t  
 ORIGIN

RESULT 3  
 AR043683/c  
 LOCUS AR043683  
 DEFINITION Sequence 53 from patent US 5814517.  
 ACCESSION AR043683  
 VERSION AR043683.1 GI:5964691  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Seidel, H. Martin and Lamb, I. Peter.  
 TITLE DNA spacer regulatory elements responsive to cytokines and methods for their use  
 JOURNAL Patent: US 5814517-A 29-SEP-1998;  
 FEATURES Location/Qualifiers  
 source 1..10 /organism="unknown" 1 g 4 t  
 BASE COUNT 4 a 1 c 1 g 4 t  
 ORIGIN

RESULT 4  
 AR097294  
 LOCUS AR097294 11 bp DNA  
 DEFINITION Sequence 17 from patent US 6071700.  
 ACCESSION AR097294  
 VERSION AR097294.1 GI:12806024  
 KEYWORDS  
 SOURCE Unknown.

Query Match 82.2%; Score 7.4; DB 9; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 1.6e+09; Mismatches 1;  
 Matches 8; Conservative 0; Indels 0; Gaps 0;  
 Oy 1 ttctgagaa 9  
 ||||| 1  
 Db 9 TTCTGGAA 1

RESULT 1  
 AX041991  
 LOCUS AX041991 9 bp DNA  
 DEFINITION Sequence 21 from Patent WO005067.  
 ACCESSION AX041991  
 VERSION AX041991.1 GI:11340754  
 KEYWORDS human.  
 SOURCE  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 9)  
 AUTHORS Nelson, P.S., Hood, L. and Lin, B.  
 TITLE Prostate-specific polynucleotides, polypeptides and their methods  
 of use  
 JOURNAL Patent: WO 005067-A 21 NOV-2000;  
 FEATURES Location/Qualifiers  
 source  
 BASE COUNT 3 a /bound\_moiety="Interleukin response element binding site"  
 ORIGIN

Query Match 82.2%; Score 7.4; DB 9; Length 10;  
 Best Local Similarity 88.9%; Pred. No. 1.2e+06; Mismatches 1;  
 Matches 8; Conservative 0; Indels 0; Gaps 0;  
 Oy 1 ttctgagaa 9  
 /bound\_moiety="Interleukin response element binding site"  
 Db 10 TTCTTAGAA 2

RESULT 2  
 AR097294  
 LOCUS AR097294 11 bp DNA  
 DEFINITION Sequence 17 from patent US 6071700.  
 ACCESSION AR097294  
 VERSION AR097294.1 GI:12806024  
 KEYWORDS  
 SOURCE Unknown.

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REFERENCE	1 (bases 1 to 11)		1..11	
AUTHORS	He, F. and Jacobson, A.S.		/organism="synthetic construct"	
TITLE	Heterologous polypeptide production in the absence of		/db_xref="taxon:32630"	
JOURNAL	nonsense-mediated mRNA decay functions		/note="Synthetic"	
FEATURES	Patent: US 6071700-A 17-JUN-2000;			
BASE COUNT	Location/Qualifiers			
ORIGIN	1..11			
QY	1 ttctggaa 9			
Db	2 TCTGGAA 10			
RESULT	5			
AX063653	AX063653 11 bp DNA	PAT	24-JAN-2001	
LOCUS	AX063653 11 bp DNA			
DEFINITION	Sequence 37 from Patent WO0100817.			
ACCESSION	AX063653			
VERSION	AX063653.1			
KEYWORDS	GI:12541377			
ORGANISM	synthetic construct.			
REFERENCE	synthetic construct.			
AUTHORS	artificial sequence.			
TITLE	Morgan,A.R. and Severini,A.			
JOURNAL	Compositions and methods for determining the activity of			
FEATURES	dna-binding proteins and of initiation of transcription			
BASE COUNT	Patent: WO 0100817-A 37-04-JAN-2001;			
ORIGIN	DNAB Diagnostics, Inc. (CA)			
QY	1..11 <db_xref="Taxon:32630"> <note="Synthetic">			
Db	2 a 1 c 3 g 5 t			
RESULT	5			
AX063653	AX063653 11 bp DNA	PAT	24-JAN-2001	
LOCUS	AX063653 11 bp DNA			
DEFINITION	Sequence 37 from Patent WO0100817.			
ACCESSION	AX063653			
VERSION	AX063653.1			
KEYWORDS	GI:12541377			
ORGANISM	synthetic construct.			
REFERENCE	synthetic construct.			
AUTHORS	artificial sequence.			
TITLE	Morgan,A.R. and Severini,A.			
JOURNAL	Compositions and methods for determining the activity of			
FEATURES	dna-binding proteins and of initiation of transcription			
BASE COUNT	Patent: WO 0100817-A 40-04-JAN-2001;			
ORIGIN	DNAB Diagnostics, Inc. (CA)			
QY	1 ttctggaa 9			
Db	10 TCTGGAA 2			
RESULT	7			
139722	139722 11 bp DNA	PAT	13-MAY-1997	
LOCUS	139722 11 bp DNA			
DEFINITION	Séquence 9 from Patent US 5616489.			
ACCESSION	139722			
VERSION	139722.1			
KEYWORDS	GI:2084202			
ORGANISM	Unknown.			
REFERENCE	Unknown.			
AUTHORS	Unclassified.			
TITLE	Levy,D.E.			
JOURNAL	DNA sequence which binds transcriptional regulatory proteins			
FEATURES	activated in response to various cytokines and uses thereof			
BASE COUNT	Patent: US 5616489-A 9-01-APR-1997;			
ORIGIN	Location/Qualifiers			
QY	1 ttctggaa 9			
Db	2 TCTGGAA 10			
RESULT	8			
155839	155839 11 bp DNA	PAT	07-OCT-1997	
LOCUS	155839 11 bp DNA			
DEFINITION	Sequence 9 from Patent US 5648217.			
ACCESSION	155839			
VERSION	155839.1			
KEYWORDS	GI:2476633			
ORGANISM	Unknown.			
REFERENCE	Unknown.			
AUTHORS	Unclassified.			
TITLE	Levy,D.E.			
JOURNAL	DNA sequence which binds transcriptional regulatory proteins			
FEATURES	activated in response to various cytokines and uses thereof			
BASE COUNT	Patent: US 5648217-A 9-15-JUL-1997;			
ORIGIN	Location/Qualifiers			
QY	1 ttctggaa 9			
Db	2 TCTGGAA 10			
RESULT	8			
155839	155839 11 bp DNA	PAT	07-OCT-1997	
LOCUS	155839 11 bp DNA			
DEFINITION	Sequence 9 from Patent US 5648217.			
ACCESSION	155839			
VERSION	155839.1			
KEYWORDS	GI:2476633			
ORGANISM	Unknown.			
REFERENCE	Unknown.			
AUTHORS	Unclassified.			
TITLE	Levy,D.E.			
JOURNAL	DNA sequence which binds transcriptional regulatory proteins			
FEATURES	activated in response to various cytokines and uses thereof			
BASE COUNT	Patent: US 5648217-A 9-15-JUL-1997;			
ORIGIN	Location/Qualifiers			
QY	1 ttctggaa 9			
Db	2 TCTGGAA 10			
RESULT	8			
155839	155839 11 bp DNA	PAT	07-OCT-1997	
LOCUS	155839 11 bp DNA			
DEFINITION	Sequence 9 from Patent US 5648217.			
ACCESSION	155839			
VERSION	155839.1			
KEYWORDS	GI:2476633			
ORGANISM	Unknown.			
REFERENCE	Unknown.			
AUTHORS	Unclassified.			
TITLE	Levy,D.E.			
JOURNAL	DNA sequence which binds transcriptional regulatory proteins			
FEATURES	activated in response to various cytokines and uses thereof			
BASE COUNT	Patent: US 5648217-A 9-15-JUL-1997;			
ORIGIN	Location/Qualifiers			
QY	1 ttctggaa 9			
Db	2 TCTGGAA 10			
RESULT	8			
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ACCESSION	155839			
VERSION	155839.1			
KEYWORDS	GI:2476633			
ORGANISM	Unknown.			
REFERENCE	Unknown.			
AUTHORS	Unclassified.			
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Db	2 TtCTGGAA 10				
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DEFINITION beta-hexosaminidase A {exon 8}	[human, mRNA Partial Mutant, 12 nt].				
ACCESSION S75371.1	GI:241964				
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE 1 (bases 1 to 12)	Akli,S., Cheilly,J., Lacorte,J.M., Poenaru,L. and Kahn,A.				
TITLE	Seven novel Tay-Sachs mutations detected by chemical mismatch cleavage of PCR-amplified cDNA fragments				
JOURNAL	Genomics 11 (1), 124-134 (1991)				
MEDLINE	92112203				
REMARK	GenBank Staff at the National Library of Medicine created this entry [NCBI gibbsq 75371] from the original journal article. This sequence comes from Figure 4.D.				
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Db	4 TTCTAGAA 12				
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DEFINITION Sequence 516 from Patent US 6083695.					
ACCESSION AR101594					
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KEYWORDS	Unknown.				
SOURCE	Unclassified.				
REFERENCE 1 (bases 1 to 8)	Hardin,S,Houck, Honayouni,R. and Hardin,P,Eric.				
AUTHORS	Optimized primer library for gene sequencing and method of using same				
TITLE	Patent: US 6083695,A 516 04-JUL-2000;				
JOURNAL	Location/Qualifiers				
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DEFINITION Sequence 18 from Patent WO9416928.					
ACCESSION A41392					
VERSION A41392.1	GI:2297111				
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	synthetic construct.				
REFERENCE 1 (bases 1 to 10)	artificial sequence.				
AUTHORS	Strauss,M. and Bauer,D.				
TITLE	COMPLEX DIAGNOSTIC AGENT OF GENETIC EXPRESSION AND MEDICAL				
	DIAGNOSIS AND GENE ISOLATION PROCESS USING SAID DIAGNOSTIC AGENT				
JOURNAL	Patent: WO 9426928-A 18 24-NOV-1994;				
MEDLINE	MAX PLANCK GESELLSCHAFT (DE) GESellschaft für Biowissenschaften und Biotechnologie				
REMARK	COMMENT Other publication DE 4317414 940421.				
JOURNAL	GENBANK STAFF AT THE NATIONAL LIBRARY OF MEDICINE CREATED THIS ENTRY [NCBI gibbsq 75371] FROM THE ORIGINAL JOURNAL ARTICLE.				
MEDLINE	This sequence comes from Figure 4.D.				
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BASE COUNT	3 a 3 c 2 g 2 t				
ORIGIN					
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 Db 9 TCTGAGA 3

RESULT 13  
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 LOCUS A24764 11 bp DNA  
 DEFINITION oligonucleotide PS39.  
 ACCESSION A24764  
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 KEYWORDS synthetic construct.  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS Title  
 JOURNAL Patent: WO 9309218-A 4 13-MAY-1993;  
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BASE COUNT 3 a 3 c 2 g 3 t  
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 Matches 7; Conservative 0; Mismatches 0;  
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QY 3 ctgaaa 9  
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 Db 11 CTGAGAA 5

RESULT 14  
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 LOCUS AR074369 11 bp DNA  
 DEFINITION Sequence 4 from patent US 5952547.  
 ACCESSION AR074369  
 VERSION AR074369.1 GI:10001124  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1. (bases 1 to 11)  
 AUTHORS Cornelissen,M., Soetaert,P., Stijn,M., Dockx,J. and Van Aarsen,R.  
 TITLE Modified *Bacillus thuringiensis* genes with improved expression in  
 plant cells, methods of production on and use  
 JOURNAL Patent: US 5952547-A 4 14-SEP-1999;  
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 BASE COUNT 3 a 3 c 2 g 3 t  
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 ACCESSION A06058  
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QY 3 ctgaaa 9  
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 Db 3 TCTGAGA 9

KEYWORDS synthetic construct.  
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 REFERENCE 1 (bases 1 to 12)  
 AUTHORS Hudson,P.J., Haley,J.D., Niall,H.D. and Shine,J.  
 TITLE Molecular cloning and characterization of the gene sequence coding  
 for porcine relaxin  
 JOURNAL Patent: EP 0086649-A 8 24-AUG-1983;  
 HOWARD FLOREY INSTITUTE OF EXPERIMENTAL PHYSIOLOGY AND MEDICINE  
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GenCore version 4.5
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Title: SHORT
Perfect score: 9
Sequence: 1 ttctgagaa 9

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CC sequencing consortium of the German Genome Project.  
 CC No s1 sequence available.  
 CC This clone is available at the RZPD in Berlin.  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

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XX	DT 12-MAR-1999 (Rel. 59, Created) DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)	
XX	DE Homo sapiens mRNA; EST DKFZp434H0321_r1 (from clone DKFZp434H0321)	
XX	KW EST; expressed sequence tag.	
OS	Homo sapiens (human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
XX	RN [1] RN 1..11 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.; RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases. RL MIFS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY	
XX	CC clone from S. Wiemann, sequenced by LMU within the cDNA sequencing consortium of the German Genome Project	
CC	No s1 sequence available	
CC	This clone is available at the RZPD in Berlin.	
CC	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de	
XX	Key location/Qualifiers	
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QY	1 ttctgta 6       Db 3 TTCGGA 8
XX	RESULT 8 ID AW250935 AW250935 11 bp mRNA NIH_MCG_7 Homo sapiens cDNA clone EST 07-JAN-2000 IMAGE:2821359 3', mRNA sequence.

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 VERSION AW250935.1  
 KEYWORD EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS NIH-MGC  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Other\_ESTs: 2821359\_Sprime  
 Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 Tissue Procurement: DCTD/DPG cDNA Library Preparation: LING  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LINC) DNA Sequencing by: Berkeley MGC sequencing  
 project. Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LINC at:  
[www.bio.llnl.gov/bbpc/image.html](http://www.bio.llnl.gov/bbpc/image.html)  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu>  
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 cloned into EcoRI/XbaI sites using the following 5'  
 adaptor: GCA CGA G (G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
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 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
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 XX EST; expressed sequence tag.  
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 XX  
 RN [1]  
 RP 1-12  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RT ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by LMU within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No sl sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 RP 1-12  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RT ; Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by LMU within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No sl sequence available

CC	This clone is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: cloneer@rzpd.de									
CC										
CC										
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LOCUS	GSSC07954	Trypanosoma cruzi random genomic library	Trypanosoma							
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ACCESSION	AQ909961									
VERSION	AQ909961.2	GI:9371014								
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REFERENCE	Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.	Genome Res. 10 (12), 1996-2005 (2000)	JOURNAL	COMMENT						
AUTHORS	1 (bases 1 to 5)		MEDLINE							
TITLE	A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery	Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral San Martin)	REFERENCE	Agüero, F., Verdún, R., Frasch, A.C.C. and Sanchez, D.O.						
JOURNAL	Genome Res. 10 (12), 1996-2005 (2000)	Av. Gral Paz entre Albarellos Y Constituyentes, INTI edificio 24 CP(1650) San Martin, Prov. de BS AS. Argentina	AUTHORS	A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery						
MEDLINE	2056849	Tel: 54-11-4580-7255 ext 309	TITLE	Fax: 54-11-4752-9539						
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BASE COUNT	4 a	0 c	1 g	0 t						
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	JOURNAL									
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	Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral San Martin)									
	Av. Gral Paz entre Albarellos Y Constituyentes, INTI edificio 24 CP(1650) San Martin, Prov. de BS AS. Argentina									
	Tel: 54-11-4580-7255 ext 309									
	Fax: 54-11-452-9639									
	Email: dsanchez@ib.unsam.edu.ar									
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 adapter: GCAACGG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
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